

FIG. 1A

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTCGACCCACGCGTCCGACTCAACAATGCTGCCCTCTCTGACTGCACCGTCCCGCCGCGCTGCCGCGCGGCC	79
CAAGCCAAAGTCGAGCGGGGCGTTGCCACCGACGGCACAGCCCTTGGGCCCGCCGGGACCAAGAGGTAGCCGCGG	158
CGCACAGCTCCGTCGCGCTCGCCCGTCTGAGCGCCCGCAGGTGCCCCGAGCCCGCCCGGAG ATG CAC AGC CCG	233
P G L L A L W L C A V L C A S A R G G S	24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGC GGC AGC	293
D P Q P G P G R P A C P A P C H C Q E D	44
GAC CCC CAG CCT GGC CCG GCG CGT CCC GCC TGC CCG GCT TGC CAC TGC CAG GAG GAC	353
G I M L S A D C S E L G L S V P A D L	64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG	413
D P L T A Y L D L S M N N L T E L Q P G	84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT	473
L F H H L R F L E E L R L S G N H L S H	104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTC CGG CTC TCA GGC AAC CAC CTC TCA CAC	533
I P G Q A F S G L H S L K I L M L Q S N	124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC	593

FIG.1B

Q	L	R	G	I	P	A	E	A	L	W	E	L	P	S	L	Q	S	L	R	144
CAG	CTC	CGT	GGG	ATC	CCA	GCA	GAG	GCA	CTA	TGG	GAG	CTG	CCC	AGC	CTG	CAG	TCG	CTG	CGC	653
L	D	A	N	L	I	S	L	V	P	E	R	S	F	E	G	L	S	S	L	164
CTA	GAT	GCT	AAT	CTC	ATC	TCC	CTG	GTC	CCT	GAG	AGA	AGC	TTT	GAG	GGG	CTC	TCC	TCC	CTC	713
R	H	L	W	L	D	D	N	A	L	T	E	I	P	V	R	A	L	N	N	184
CGC	CAC	CTC	TGG	CTG	GAT	GAC	AAT	GCA	CTC	ACT	GAG	ATC	CCC	GTC	AGA	GCT	CTC	AAC	AAC	773
L	P	A	L	Q	A	M	T	L	A	L	N	H	I	R	H	I	P	D	Y	204
CTT	CCT	GCC	CTA	CAG	GCC	ATG	ACC	TTG	GCT	CTC	AAC	CAT	ATC	CGC	CAC	ATC	CCT	GAC	TAT	833
A	F	Q	N	L	T	S	L	V	V	L	H	L	H	N	N	R	I	Q	H	224
GCC	TTC	CAG	AAC	CTC	ACC	AGT	CTT	GTG	GTG	CTG	CAT	CTA	CAT	AAC	AAC	CGC	ATC	CAG	CAT	893
V	G	T	H	S	F	E	G	L	H	N	L	E	T	L	D	L	N	Y	N	244
GTG	GGG	ACC	CAC	AGC	TTC	GAG	GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAC	TAT	AAT	953
E	L	Q	E	F	P	L	A	I	R	T	L	G	R	L	Q	E	L	G	F	264
GAG	CTG	CAG	GAG	TTC	CCC	TTG	GCT	ATC	CGG	ACC	CTG	GGC	AGG	CTG	CAG	GAA	TTG	GGT	TTC	1013
H	N	N	N	I	K	A	I	P	E	K	A	F	M	G	N	P	L	L	Q	284
CAT	AAC	AAC	AAC	ATC	AAG	GCT	ATC	CCA	GAG	AAA	GCC	TTC	ATG	GGC	AAC	CCT	CTC	CTG	CAG	1073
T	I	H	F	Y	D	N	P	I	Q	F	V	G	R	S	A	F	Q	Y	L	304
ACA	ATA	CAT	TTT	TAT	GAC	AAC	CCA	ATC	CAG	TTT	GTG	GGA	AGG	TCA	GCA	TTC	CAG	TAC	CTG	1133

FIG. 1C

S	K	L	H	T	L	S	L	N	G	A	T	D	I	Q	E	F	P	D	L		324
TCT	AAA	CTG	CAT	ACG	CTA	TCT	TTG	AAT	GGT	GCC	ACT	GAT	ATC	CAA	GAG	TTC	CCA	GAC	CTC		1193
K	G	T	T	S	L	E	I	L	T	L	T	R	A	G	I	R	L	L	P		344
AAA	GGC	ACC	ACT	AGC	CTG	GAG	ATC	CTG	ACC	CTG	ACC	CGT	GCG	GGC	ATC	AGA	CTG	CTC	CCA		1253
P	G	V	C	Q	Q	L	P	R	L	R	I	L	E	L	S	H	N	Q	I		364
CCG	GGA	GTG	TGC	CAA	CAG	CTG	CCT	AGG	CTC	CGA	ATC	CTG	GAG	CTG	TCT	CAT	AAT	CAG	ATC		1313
E	E	L	P	S	L	H	R	C	Q	K	L	E	E	I	G	L	R	H	N		384
GAG	GAG	TTA	CCC	AGC	CTG	CAC	AGA	TGT	CAG	AAG	CTG	GAG	GAA	ATT	GGC	CTC	CGA	CAT	AAC		1373
R	I	K	E	I	G	A	D	T	F	S	Q	L	G	S	L	Q	A	L	D		404
AGG	ATC	AAG	GAA	ATT	GGT	GCA	GAT	ACC	TTC	AGC	CAG	CTG	GGC	TCC	TTG	CAA	GCT	TTA	GAC		1433
L	S	W	N	A	I	R	A	I	H	P	E	A	F	S	T	L	R	S	L		424
CTG	AGT	TGG	AAT	GCC	ATC	CGT	GCC	ATC	CAC	CCT	GAG	GCT	TTC	TCA	ACC	CTT	CGA	TCC	TTG		1493
V	K	L	D	L	T	D	N	Q	L	T	T	L	P	L	A	G	L	G	G		444
GTT	AAG	CTG	GAC	CTG	ACT	GAC	AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGG	CTG	GGA	GGC		1553
L	M	H	L	K	L	K	G	N	L	A	L	S	Q	A	F	S	K	D	S		464
CTG	ATG	CAC	CTG	AAG	CTC	AAA	GGG	AAC	TTG	GCC	CTG	TCT	CAG	GCC	TTC	TCC	AAG	GAC	AGT		1613
F	P	K	L	R	I	L	E	V	P	Y	A	Y	Q	C	C	A	Y	G	I		484
TTC	CCA	AAA	CTG	AGG	ATC	CTG	GAG	GTG	CCC	TAC	GCC	TAC	CAG	TGC	TGT	GCC	TAC	GGC	ATC		1673

FIG.1D

C	A	S	F	F	K	T	S	G	Q	W	Q	A	E	D	F	H	P	E	E	504
TGT	GCC	AGC	TTC	TTC	AAG	ACC	TCT	GGG	CAG	TGG	CAG	GCC	GAG	GAC	TTT	CAT	CCA	GAA	GAA	1733
E	E	A	P	K	R	P	L	G	L	L	A	G	Q	A	E	N	H	Y	D	524
GAG	GAG	GCA	CCA	AAG	AGG	CCC	CTG	GGT	CTC	CTT	GCT	GGA	CAA	GCT	GAG	AAC	CAC	TAT	GAC	1793
L	D	L	D	E	L	Q	M	G	T	E	D	S	K	P	N	P	S	V	Q	544
CTA	GAC	CTG	GAT	GAG	CTC	CAG	ATG	GGG	ACA	GAG	GAC	TCA	AAG	CCA	AAC	CCC	AGT	GTC	CAG	1853
C	S	P	P	V	P	G	P	F	K	P	C	E	H	L	F	E	S	W	G	564
TGC	AGC	CCT	GTT	CCA	GGC	CCC	TTC	AAG	CCC	TGC	GAG	CAC	CTC	TTT	GAG	AGC	TGG	GGC	ATC	1913
R	L	A	V	W	A	I	V	L	L	S	V	L	C	N	G	L	V	L	L	584
CGC	CTT	GCT	GTG	TGG	GCC	ATC	GTG	CTG	CTC	TCC	GTA	CTC	TGT	AAC	GGG	CTG	GTG	CTG	CTG	1973
T	V	F	A	S	G	P	S	P	L	S	P	V	K	L	V	V	G	A	M	604
ACA	GTC	TTT	GCC	AGC	GGA	CCC	AGC	CCG	CTG	TCC	CCC	GTC	AAG	CTT	GTG	GTG	GGT	GCG	ATG	2033
A	G	A	N	A	L	T	G	I	S	C	G	L	L	A	S	V	D	A	L	624
GCA	GGC	GCC	AAC	GCC	CTG	ACG	GGC	ATT	TCC	TGT	GGT	CTC	CTG	GCC	TCT	GTG	GAC	GCC	TTG	2093
T	Y	G	Q	F	A	E	Y	G	A	R	W	E	S	G	L	G	C	Q	A	644
ACC	TAT	GGT	CAG	TTC	GCT	GAG	TAT	GGA	GCC	CGC	TGG	GAG	AGC	GGT	CTG	GGC	TGC	CAG	GCT	2153
T	G	F	L	A	V	L	G	S	E	A	S	V	L	L	L	T	L	A	A	664
ACG	GGC	TTC	CTG	GCT	GTC	CTG	GGT	TCA	GAG	GCG	TCG	GTG	CTG	CTG	CTC	ACA	CTG	GCG	GCC	2213

FIG. 1E

V	Q	C	S	I	S	V	T	C	V	R	A	Y	G	K	A	P	S	P	G	684
GTG	CAG	TGC	AGC	ATC	TCT	GTG	ACC	TGC	GTC	CGA	GCC	TAC	GGG	AAG	GCG	CCG	TCG	CCT	GGC	2273
S	V	R	A	G	A	L	G	C	L	A	L	A	G	L	A	A	A	L	P	704
AGC	GTC	CGC	GCA	GGC	GCA	CTG	GGA	TGC	CTG	GCG	CTG	GCC	GGG	CTG	GCC	GCA	GCA	CTG	CCG	2333
L	A	S	V	G	E	Y	G	A	S	P	L	C	L	P	Y	A	P	P	E	724
CTG	GCC	TCG	GTG	GGA	GAG	TAT	GGC	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCC	CCA	CCC	GAG	2393
G	R	P	A	A	L	G	F	A	V	A	L	V	M	M	N	S	L	C	F	744
GGC	CGG	CCG	GCC	GCC	CTG	GGC	TTC	GCT	GTA	GCC	CTG	GTG	ATG	ATG	AAC	TCG	CTC	TGC	TTC	2453
L	V	V	A	G	A	Y	I	K	L	Y	C	D	L	P	R	G	D	F	E	764
CTG	GTG	GTG	GCC	GGC	TAC	ATC	ATC	AAG	CTC	TAC	TGT	GAC	CTG	CCA	CGG	GGT	GAC	TTT	GAG	2513
A	V	W	D	C	A	M	V	R	H	V	A	W	L	I	F	A	D	G	L	784
GCC	GTG	TGG	GAC	TGC	GCC	ATG	GTG	CGC	CAC	GTG	GCC	TGG	CTC	ATC	TTT	GCA	GAT	GGC	CTC	2573
L	Y	C	P	V	A	F	L	S	F	A	S	M	L	G	L	F	P	V	T	804
CTC	TAC	TGC	CCC	GTG	GCC	TTC	CTC	AGC	TTT	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACC	2633
P	E	A	V	K	S	V	L	L	V	V	L	P	L	P	A	C	L	N	P	824
CCC	GAG	GCT	GTC	AAG	TCA	GTC	CTT	CTG	GTG	GTG	CTG	CCT	CTG	CCT	GCC	TGC	CTC	AAC	CCA	2693
L	L	Y	L	L	F	N	P	H	F	R	D	D	L	R	R	L	W	P	S	844
CTG	CTC	TAC	CTG	CTC	TTC	AAC	CCT	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTC	TGG	CCA	AGC	2753

FIG. 1E

P	R	S	P	G	P	L	A	Y	A	A	A	G	E	L	E	K	S	S	C	864
CCT	CGG	TCC	CCA	GGG	CCC	CTA	GCC	TAC	GCT	GCA	GCC	GGT	GAG	CTG	GAG	AAG	AGC	TCC	TGC	2813

[illegible][illegible]

H	Q	P	G	A	T	R	L	E	G	N	H	F	I	E	S	D	G	T	K
CAT	CAG	CCG	GGG	GCC	ACC	AGG	CTG	GAG	GGA	AAC	CAT	TTT	ATA	GAG	TCT	GAT	GGA	ACC	AAG

F	G	N	P	Q	P	P	M	K	G	E	L	L	K	A	E	G	A	T
TTT	GGG	AAC	CCA	CAA	CCT	CCC	ATG	AAG	GGA	GAA	CTG	CTG	AAG	GCA	GAG	GGA	GCC	ACT

L	A	G	C	G	S	S	V	G	G	A	L	W	P	S	G	S	L	F	A
TTG	GCA	GGC	TGT	GGC	TCT	TCC	GTG	GGT	GGA	GCC	CTC	TGG	CCC	TCT	GGC	TCT	CTC	TTT	GCC

S	H	L	*	968
TCT	CAC	TTG	TAA	3125

ATATCCCTCTCTGTTTGTCTCTCCCATCCCAATGATGGCTGCTTATAAAGAAAGACAACCTCCACTCCATAGCAAGA 3204

TGGCCAAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGCTCTTGG 3283

CCTTCAGCCTTCACTTCAACCCCTGGGCCCTTCTCTGTCCAATCCAAATACTTGACAGAGGCCCTGGGAAAATTGCATAGGA

FIG.1G

GAAAGGAGAAAAGCAAAGACAGTGAAGGTTATTGGGGCCCTGACAGAGCCATGATCAGTAAAGTGCAGAGTGTGGGAG 3441

GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCCTGTGACATATAGAAATATAAAATG 3520

TGTTCTGCGTTCATTAATCTTGACCTATGCTGNGCCAAAAGTGCTTCCGTAAATAACACTTTGGAAAGACATTGAAAA 3599

AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637

??

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+
 ftmzb048h1
 67 LTAYLDLSMNNTLQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ L+ N+L+++p++al+ Lp+L++L L+ N ++ +p++++f++L+
 ftmzb048h1
 115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSEFGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L++L+L++N Lt++p al+nLp L+ L N+++++p+++fqnl+
 ftmzb048h1
 163 SLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L +L+L nN+++++ +++++L+nLe+LdL++N+L+++p ++L+
 ftmzb048h1
 211 SLVVLHLHNNRIQHVGTSHSEGLHNLETLDLNYNELQEFPPL-AIRTLG 257

FIG.2B

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
 ftmzb048h1
 258 RLQELGFHNNNIKAIPKAFMGNPLQLQTIHFYDNPQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L++L+L++ ++++++p+ |++ ++Le L L + ++ lppg++q L+
 ftmzb048h1
 306 KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ L+Ls+N+++++lp+ |+ +++Lee+ L +N+++++ ++f+ L+
 ftmzb048h1
 353 RLRILELSHNQIEELPS--LHRCQKLEELRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
 ftmzb048h1
 399 SLQALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTPLAGLGGLM 446

FIG. 3A-1

Protein (species)*	Function-Igand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α2-GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF-β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexner)	?-?	?
IpaH4.5 (Shigella flexner)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence	PIR entry
15	28 (A)	.LE.L.L..C-.LT...C..L..aL....	A31857
	29 (B)	.L.EL.L..N-.LGD.Ga..L...L..P..	
8	24	.L..L.L..N-.L..-L...LL....--.	NBHUA2
8	29	.L..L.L..N-.a.....a.....	BVBYN1
4	24	.L..L.a..N-.a.....L--.	S03616
8	24	.L..L.L..N-.I..-a....a....--.	A40757
10	24	.L..L.L..N-.I..-V....a....--.	NBHUC8
11	24	.L..L.L..N-.a....a....--.	S05390
12	24	.L..L.L..N-.L..-....a....--.	A41748
6	24	.L..a.L..N-.I..-....a....--.	A41781
6	24	.L..a.L..N-.a..-....F....--.	A35272
7	24	.L..L.L..N-.L..-LP.GL...L--.	NBHUIA
14	24	.L..L.L..N-.L..-LP..LF..L--.	-
12	20	.L..L.a..N-.L..-LP-..----L--PP	A33950
6	20	.L..L.V..N-.L..-LP-..----L--P.	A35149
8	20	.L..L.a..N-.L..-LP-..----L--P.	S18248
19	24	.L..L.L..N-.L..-....F....--.	A29943
19	24	.L..L.L..N-.I..-....F..L--.	A36665
7	24	.L..LNL..N-.I..-a....aF..L--.	S28464
30	24	.L..L.L..N-.a..-a....F..a--.	A29944
16	23	.L..L.LS.N-.L..-aP..a..-L--.	-
8	24	.L..L.LSNN-.a..-a.....L--.	A34210

FIG. 3B-1

Protein (species)*	Function-ligand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces Cerevisiae)	Signal transduction-RAS	PM (cytoplasm)
T-LR (Tyrpanosoma brucei)	?-?	?
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?
DRT100 (Arabidopsis thaliana)	Recombination-?	Chloroplast
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus
p34 ribosome-binding protein (rat)	RM membranes-ribosome	RM membrane (cytoplasm)
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma
Intermalin (Listeria monocytogenes)	Invasion-?	Cell wall
InIB (Listeria monocytogenes)	?-?	?
LRR superfamily		

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L.L..N-.....	TDHUM4
2	23	.L..LS.N-.L.....	TVHUTT
3	23	.L..LaT.N-.LTS.....	S06943
3	23	.LR.aNLSQN-.L..S.....	A40026
11	23	.L..a.L..N...G.aP-.a.SL--.	JQ1674
5	25	.L..L.a..T-.a.....F.....	A41343
7	25	.L..L.aS.T-....LP...a.a--.	A34548
6	25	.a..L.a.NN..a.S-a.....a--.	A40077
20	23	.L..L.L..N-.a...-a...L--.	OYBY
18	23	.L..L.LSGC..a...-a...L--.	A36359
3	23	.a.LaDI..N--LP..a.....N---	DDBYD1
5	26	.L..L.a..C..a...a...a...-P	A25226
5	24	.L..LNL..N-.L.G.IP.S-a.S---	A46260
9	26	.L..a.L..C.NaTD..a...L..L--.	A41529
4	23	.L..L.a..N-.LT.-LP.E-a...--.	S31286
11	22	.L..L.a..N-.I...-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L...-LP...F..L--.	-
12	24	.L..L.L..N-.L...-LP..aF..L--.	A34901
13	22	NL..L.L..n-QISDI.P---L..L--T	A39930
6	22	.L..L.L..N-.L.DI...-L..L--.	C39930
	5	10 15 20 25	
		.L..L.L..N*.a..*a****a**a**.	

FIG. 4

>human DNA seq.

TAATACGACTCACTATAGGGAAAGCTGGTACGCCTG AAGGTACCGGTCCGGAA
TTCCCGGGTTCGACCCACGCGTCCGTGGAGCGGAGC CAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTC CAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTC CCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGC CCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTC ACCACACTGCCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGG GAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAACCTGAGGA TCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCT TCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAG GAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTA TGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACAC CCAAGTGTCCAGTGTAGC
CCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTC TTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTGCTCTCCG TGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCC CCGTGGCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACT GGCATTTCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTT CTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGGCCACTGG CTTCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCG CAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGGCCTATGGGAAGTCCC CCTCCCTGGGCAGCGTTCC
AGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCT GGCCGCCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCA CTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACC GTGGCCCTGGTGTATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCT ACATCAAACCTGTACTGTGA
CCTGCCGCGGGGGCGACTTTGAGGCCGTGTGGGACT GCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGGCTCCTCTA CTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGGCCTCTTCCCTGTCA CGCCCGAGGCCGTCAAGT
CTGTCTGCTGGTGGTGTGCTGCCCTGCCTGCCTGC CTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGG CGGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCC GGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT GATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGGCCCCCTGGGCTGG GAGACCTATGGCTTCCCCCTC
AGTGACCCTCATCTCCTGTGTCAGCAGCCAGGGGG CCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAAC CCCCCAACCTCCATGGA
TGGAGAAGTGTGCTGCTGAGGGCAGAGGGATCTACG CCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGC CTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTTCCCCCTCTTCCC ITTCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAACAAATACAACCAA AACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCAC CTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGG CCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCTTGTGTCATGTCTGAAGCT GTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGAC AGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGA GAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATG TGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAA TAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAAAGGGCGGCGCTCTAGAGGATC CAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTACCTAA ATTCAATT

SCANNED # 2

FIG. 5

>fahr human

NTTHRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTPLAGLGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCYL
FESWGIRLAWWAINLLSVLNCNGLVLLTVFAGGPAPLPPVKFVGAAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRTATGFLAVLGSEASVLLLTAAVQC SVSVS
CVRAYGKSPSLGSRAGVLGCLALAGLAAALPLASVGEY GASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVLPACLNPLL YLLFNPHFRDDL R
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11
 *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
 +L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp + +L
 fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGG 110
 k<-*
 fahr 111 M 111

FIG. 7A

ftmzb048h10	1	MHSPGGLLALWLCASARGGSDPQPGPRPACAPCHCQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNNLTE	80
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	81	LQGLFHHLRFLLEELRLSGNHLSHIPGQAFSGLSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEG	160
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	161	LSSLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETL	240
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	241	LNYNELQEFFPLAIRTLGRLOELGFHNNNIKAIPKAFMGNPLLQTIHFYDNPIQFVGRSAFOYLSKLHTLSLNGATDIOE	320
Aa_of_aambb001d112		~~~~~	
fahr_human		~~~~~	
ftmzb048h10	321	FPDLKGTTSLEILTLTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEELGLRHNRIKEIGADTFSQLGSL	400
Aa_of_aambb001d112		~~~~~	
fahr_human		----H--ASVE-----RSQGLSLP----AHPASLAALAASNTTASG-----KLEX-----DTSFQLSSL	480
ftmzb048h10	401	QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTIPLAGLGGIMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC	480
Aa_of_aambb001d112		~~~~~	
Fahr_human		~~~~~	
ftmzb048h10	481	QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTIPLAGLGGIMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC	560
Aa_of_aambb001d112		~~~~~	
fahr_human		AYGICASFFKTSQWQAEDFHPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPGFKPCPEHLFE	
		AYGICASFFKTSQWQAEDFHPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPHPSVQCSPVPGFKPCPEHLFE	
		PYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPVPGFKPCPEYLF	

FIG. 7B

561
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 561
 SWGIRLAVWAIIVLLSVLCNGLVLLTVFASGSPSPVSVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
 SWGIRLAVWAIIVLLSVLCNGLVLLTVFASGSPSPVSVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
 SWGIRLAVWAIIVLLSVLCNGLVLLTVFAGGPAPVPPVKFVVGAIAAGANTLTGISCGLLASVDALTYGQFSEYGARWETGL

TM II

641
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 641
 GCQATGFLAVLGSEASVLLLTAAVQCSISVTCVRAVGKAPSPGSRVAGALGCIALAGLAAALPLASVGEYGASPLCLPY
 GCQATGFLAVLGSEASVLLLTAAVQCSISVTCVRAVGKAPSPGSRVAGALGCIALAGLAAALPLASVGEYGASPLCLPY
 GCRTGFLAVLGSEASVLLLTAAVQCSVSVCVRAVGKSPSLGSRVAGVLCIALAGLAAALPLASVGEYGASPLCLPY

TM IV

721
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 721
 APPEGRPAALGFAVALVMNNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIIFADGILLYCPVAFLSFASMLGL
 APPEGRPAALGFAVALVMNNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIIFADGILLYCPVAFLSFASMLGL
 APPEGQPAALGFTVALVMNNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIIFADGILLYCPVAFLSFASMLGL

TM V

801
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 801
 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLWPSRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLWPSRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL

TM VI

TM VII

881
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 881
 EASEAGQPPGLETYGFPSVTLSRHQPGATRLEGNHFIESDGTGKFNPPMPKGEILLKAEGATLAGCGSSVGGALWPSSG
 EASEAGQPPGLETYGFPSVTLSRHQPGATRLEGNHFIESDGTGKFNPPMPKGEILLKAEGATLAGCGSSVGGALWPSSG
 EASEAGRPPGLETYGFPSVTLSRQOPGAPRLEGSHCPEPEGNHFGNPPQSMGDEILLRAEGSTPAGGGLSGGGGFQPSG
 961
 SLFASHLN
 SLFASHLN
 LAFASHVN

961
 ftmzb048h10
 Aa_of_aambb001d112
 fahr_human
 961
 SLFASHLN
 SLFASHLN
 LAFASHVN

FIG.8A

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	ATC	AAG	GCC	120	
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540

FIG.8B

S	I	H	P	E	A	F	S	T	L	H	S	L	V	K	L	D	L	T	D	200
TCC	ATC	CAC	CCT	GAG	GCC	TTC	TCC	ACC	CTG	CAC	TCC	CTG	GTC	AAG	CTG	GAC	CTG	ACA	GAC	600
N	Q	L	T	T	L	P	L	A	G	L	G	G	L	M	H	L	K	L	K	220
AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGA	CTT	GGG	GGC	TTG	ATG	CAT	CTG	AAG	CTC	AAA	660
G	N	L	A	L	S	Q	A	F	S	K	D	S	F	P	K	L	R	I	L	240
GGG	AAC	CTT	GCT	CTC	TCC	CAG	GCC	TTC	TCC	AAG	GAC	AGT	TTC	CCA	AAA	CTG	AGG	ATC	CTG	720
E	V	P	Y	A	Y	Q	C	C	P	Y	G	M	C	A	S	F	F	K	A	260
GAG	GTG	CCT	TAT	GCC	TAC	CAG	TGC	TGT	CCC	TAT	GGG	ATG	TGT	GCC	AGC	TTC	TTC	AAG	GCC	780
S	G	Q	W	E	A	E	D	L	H	L	D	D	E	E	S	S	K	R	P	280
TCT	GGG	CAG	TGG	GAG	GCT	GAA	GAC	CTT	CAC	CTT	GAT	GAT	GAG	GAG	TCT	TCA	AAA	AGG	CCC	840
L	G	L	L	A	R	Q	A	E	N	H	Y	D	Q	D	L	D	E	L	Q	300
CTG	GGC	CTC	CTT	GCC	AGA	CAA	GCA	GAG	AAC	CAC	TAT	GAC	CAG	GAC	CTG	GAT	GAG	CTC	CAG	900
L	E	M	E	D	S	K	P	H	P	S	V	Q	C	S	P	T	P	G	P	320
CTG	GAG	ATG	GAG	GAC	TCA	AAG	CCA	CAC	CCC	AGT	GTC	CAG	TGT	AGC	CCT	ACT	CCA	GGC	CCC	960
F	K	P	C	E	Y	L	F	E	S	W	G	I	R	L	A	V	W	A	I	340
TTC	AAG	CCC	TGT	GAG	TAC	CTC	TTT	GAA	AGC	TGG	GGC	ATC	CGC	CTG	GCC	GTG	TGG	GCC	ATC	1020
V	L	L	S	V	L	C	N	G	L	V	L	L	T	V	F	A	G	G	P	360
GTG	TTG	CTC	TCC	GTG	CTC	TGC	AAT	GGA	CTG	GTG	CTG	ACC	GTG	TTC	GCT	GGC	GGG	CCT	1080	

FIG. 8C

A	P	L	P	P	V	K	F	V	V	G	A	I	A	G	A	N	T	L	T	380
GCC	CCC	CTG	CCC	CCG	GTC	AAG	TTT	GTG	GTA	GGT	GCG	ATT	GCA	GGC	GCC	AAC	ACC	TTG	ACT	1140
G	I	S	C	G	L	L	A	S	V	D	A	L	T	F	G	Q	F	S	E	400
GGC	ATT	TCC	TGT	GGC	CTT	CTA	GCC	TCA	GTC	GAT	GCC	CTG	ACC	TTT	GGT	CAG	TTC	TCT	GAG	1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T	G	F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GGC	TGC	CGG	GCC	ACT	GGC	TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	L	T	L	A	A	V	Q	C	S	V	S	V	440
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC	GCA	GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTT	CGA	GCA	GGG	GTC	CTA	1380
G	C	L	A	L	A	G	L	A	A	A	L	P	L	A	S	V	G	E	Y	480
GGC	TGC	CTG	GCA	CTG	GCA	GGG	CTG	GCC	GCC	GCA	CTG	CCC	CTG	GCC	TCA	GTG	GGA	GAA	TAC	1440
G	A	S	P	L	C	L	P	Y	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
I	K	L	Y	C	D	L	P	R	G	D	F	E	A	V	W	D	C	A	M	540
ATC	AAA	CTG	TAC	TGT	GAC	CTG	CCG	CGG	GGC	GAC	TTT	GAG	GCC	GTG	TGG	GAC	TGC	GCC	ATG	1620

FIG. 8D

V	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
CTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160

G	G	G	G	F	Q	P	S	G	L	A	F	A	S	H	V	*
GGG	GGT	GGC	GGC	TTT	CAG	CCC	TCT	GGC	TTG	GCC	TTT	GCT	TCA	CAC	GTG	TAA
ATATCCCTCCCCA	TTCTCTCTTCCCTCTCTTCCCTCTCTTCCCTCTCTCGGTGAATGATGGCTGCTTCTTAAAAACA	2290														
AATAACAACCAA	AACTCAGCAGTGATCTATAGCAGGATGCCCCAGTACCCTGGCTCCACTGATCACCTCTCTCCTGTGA	2369														
CCAATCACCA	ACGGGTGCCTCTTTGGCCCTGGCTTTCCCTTTGGCCCTTCCTCAGCTTCACCTTGATACTGGGCCCTCTTCTCCTTG	2448														
TCATGCTCTGA	AGCTGTGGACCAAGACCTGGACTTTTGTCTGCTTAAGGGAATGAGGGGAAGTAAAGACAGTGAAGGGG	2527														
TGGAGGGTTG	ATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAGGCCCTGGAAGGTGATTTCCTCGTGTGACTCATG	2606														
GATAGGATACA	AAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATATGCATAAAGACTTCCTATTAAAAATAAGCTT	2685														
TGGAAGAGAT	TAAAAA	2711														

PFAM

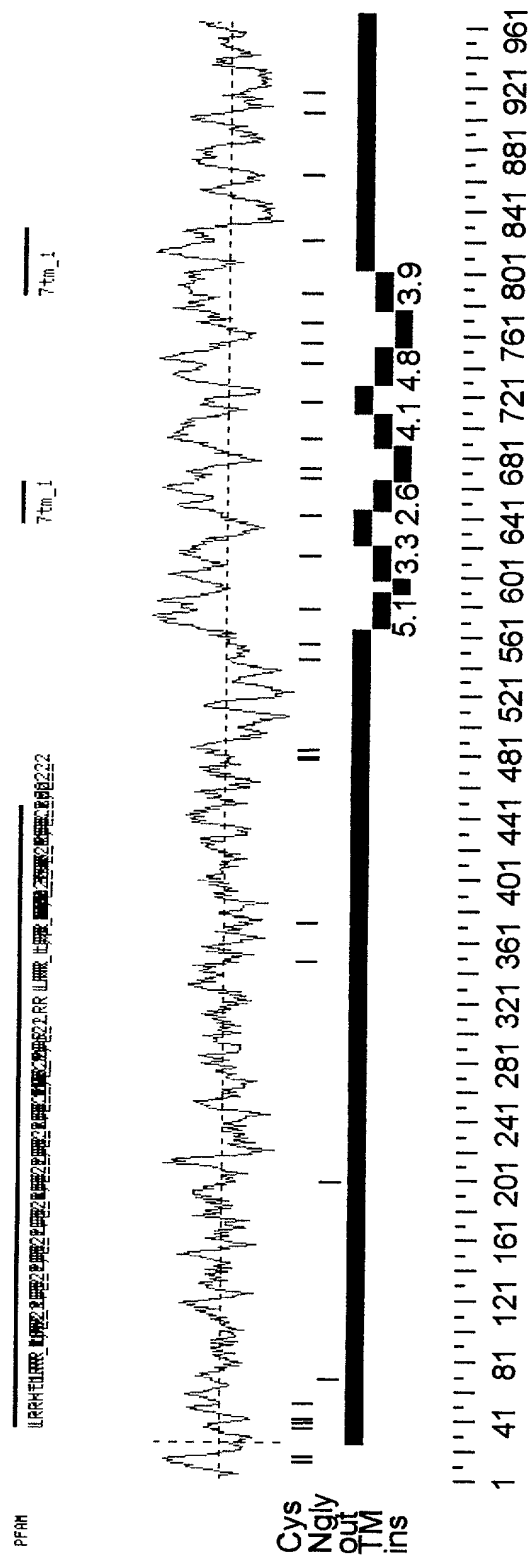


FIG. 10A

Searching for complete domains in PFAM

hmmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
<u>LRR</u>	Leucine Rich Repeat	241.4	1.3e-68	16
<u>LRRNT</u>	Leucine rich repeat N-terminal domain	27.2	0.00038	1
<u>7tm_1</u>	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65 ..	1	31 []	27.2	0.00038
LRR	1/16	67	90 ..	1	23 []	12.4	11
LRR	2/16	91	114 ..	1	23 []	24.2	0.0031
LRR	3/16	115	138 ..	1	23 []	19.9	0.062
LRR	4/16	139	162 ..	1	23 []	16.4	0.7
LRR	5/16	163	186 ..	1	23 []	27.5	0.00031
LRR	6/16	187	210 ..	1	23 []	12.1	13
LRR	7/16	211	234 ..	1	23 []	21.6	0.019
LRR	8/16	235	257 ..	1	23 []	18.2	0.2
LRR	9/16	258	281 ..	1	23 []	19.0	0.11
LRR	10/16	282	305 ..	1	23 []	10.2	32
LRR	11/16	306	328 ..	1	23 []	5.6	1.5e+02
LRR	12/16	329	352 ..	1	23 []	8.8	52
LRR	13/16	353	374 ..	1	23 []	19.2	0.097
LRR	14/16	375	398 ..	1	23 []	16.9	0.49
LRR	15/16	399	422 ..	1	23 []	23.7	0.0042
LRR	16/16	423	446 ..	1	23 []	16.4	0.66
7tm_1	1/2	635	662 ..	51	79 ..	3.4	2.2
7tm_1	2/2	784	827 ..	207	259 .]	1.1	11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-

aCp++C+C +++ l+ dCs++gL +vP dl

15088 34 ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

->nLeeLdLsnN.LtslppglfsnLp<-

+LdLs N+Lt+l pglf++L+

15088 67 LTAYLDLSMNnLTELQPGLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

->nLeeLdLsnN.LtslppglfsnLp<-

LeeL+Ls+N+L+++p +fs+L

15088 91 FLEELRLSGNhLSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ L L+nN+L ++p +++ Lp

15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L+ N ++ +p+ +f++L+

15088 139 SLQSLRLDANIISLVPERSFEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++N Lt++p +++nLp

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

->nLeeLdLsnN.LtslppglfsnLp<-

L+ L N+++++p+ +f+nL+

15088 187 ALQAMTLALNrISHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

->nLeeLdLsnN.LtslppglfsnLp<-

+L +L+L+nN++++l ++f++L

15088 211 SLVVLHLHNNrIQHLGTHSFEGH 234

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2

->nLeeLdLsnN.LtslppglfsnLp<-
 nLe+LdL++N+L+++p +++ L
 15088 235 NLETLDLNYNkLQEFPV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11

->nLeeLdLsnN.LtslppglfsnLp<-
 +L+eL ++nN+++ +p+++f + p
 15088 258 RLQELGFHNNnIKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32

->nLeeLdLsnN.LtslppglfsnLp<-
 L+++++ +N+++ + ++f+ Lp
 15088 282 LLQTIHFYDNpIQFVGRSAFQYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02

->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L++ +++++p+ +++ +
 15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52

->nLeeLdLsnN.LtslppglfsnLp<-
 +Le L L + +++ lp+g +++Lp
 15088 329 SLEILTLTRAgIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097

->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L Ls+N++++lp+ ++ ++
 15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49

->nLeeLdLsnN.LtslppglfsnLp<-
 +Lee+ L++N++ ++ ++fs+L+
 15088 375 KLEEIGLQHNrIWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042

->nLeeLdLsnN.LtslppglfsnLp<-
 +L+ LdLs N ++s++p++fs L
 15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

->nLeeLdLsnN.LtslppglfsnLp<-

+L +LdL +N+Lt+lp + +L

15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

->dWpfGsalCklvtaldvvnmyaSillLta<-

+W G ++C+ ++++l v+ + aS+lLLt+

15088 635 RWETG-LGCRATGFLAVLGSEASVLLLT 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

*->|CWlPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs

l+ P + + + +l ++ +++++++v l++ + +

15088 784 LLYCPVAFLSFASMLGIFPV-----

TPEAVKSVLLVVLPLPA 820

c|NPiIY<-*

c|NP++Y

15088 821 CLNPLLY 827

FIG. 11A

##

Searching for complete domains in SMART
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

 HMM file: /ddm/robison/smart/smart.all.hmms
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrnt1		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrnt1	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	0.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350 ..	1	24 []	3.1	29
LRR_bac_2	6/7	351	370 ..	1	20 []	14.6	1.3
LRR_PS_2	10/13	351	372 ..	1	24 []	10.8	8
LRR_sd22_2	3/5	351	372 ..	1	22 []	7.6	16
LRR_typ_2	11/14	351	373 ..	1	24 []	18.8	0.13
LRR_RI_2	4/4	351	378 ..	1	28 []	2.6	19
LRR_PS_2	11/13	373	396 ..	1	24 []	2.3	1e+02
LRR_typ_2	12/14	374	396 ..	1	24 []	6.8	10
LRR_sd22_2	4/5	397	418 ..	1	22 []	7.0	19
LRR_PS_2	12/13	397	419 ..	1	24 []	13.6	3.4
LRR_typ_2	13/14	397	420 ..	1	24 []	30.4	4.3e-05
LRR_bac_2	7/7	421	440 ..	1	20 []	5.8	18
LRR_sd22_2	5/5	421	441 ..	1	22 []	3.7	49
LRR_PS_2	13/13	421	442 ..	1	24 []	5.5	39
LRR_typ_2	14/14	421	444 ..	1	24 []	21.6	0.018

Alignments of top-scoring domains:

lrrntl1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtaVdCsgrgIttleVPldlPadttl<-
 +CPapC+C ++ ++ dCs++gL +vP dl + t +
 15088 34 ACPAPCHCQEdGIMLSADCSElGLS--AVPGDLDPILTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->LtsL.qvLdLsnNnLsGeIPsslgn<-
 L L+ +LdLs NnL+ e+ + l+
 15088 64 LDPLtAYLDLSMNNLT-ElQPGLFH 87

FIG. 11D

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFqg<-
 L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTTELQPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
 ->PpsLkeLnvsNnrLtPeL<-
 +L+eL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_ps_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLS-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
 ->npsLreLdLsnNkl.gdeGaraLaealks<-
 ++ L+eL+Ls+N+l+++ G + ++L s
 15088 89 LRFLEELRLSGNHLSHIPG--QAFSGLYS 115

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
 ->PpsLkeLnvsNnRltelPeL<-
 sLk+L +nN+L P+
 15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G + l+
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
 ->LpnLrelDlSnNqLtsLppgaFqg<-
 L +L+ L L+nNqL +P++a++
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
 ->PpsLkeLnvsNnRltelPeL<-
 psL++L+ + N ++ Pe
 15088 137 LPSLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
 15088 137 LPSLQSLRLDANLIS-LVPERSE 159

FIG. 11F

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdLsnNqLtsLppgaFqg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
 ->LpnLreLdLsnNqLtsLppgaFqg<-
 L++Lr+L L++N+Lt++P +a+++
 15088 161 LSSLRHLWLDNALT-EIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
 ->LtnLeeLdLsqNkI.....kKiENIde<-
 L+ L++L+L +N +++ + + + NL
 15088 161 LSSLRHLWLDNALT-eipVRALNNLPA 187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
 ->npsLreLdLsnNklgdeGaraL..aeaLks<-
 ++sLr L+L +N l++ +raL++ aL++
 15088 161 LSSLRHLWLDNALT-EIPVRALnnLPALQA 190

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ Lq L+ N++s +IP+ ++
 15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
 ->LpnLrelDlSnNqLtsLPpgaFqg<-
 Lp+L+ L N+++++P+ aFq+
 15088 185 LPALQAMTLALNRISHIPDYAFQN 208

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 LtsL+vL+L+nN++ s+
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
 ->LpnLrelDlSnNqLtsLPpgaFqg<-
 L++L +L+L+nN++++L F+g
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
 ->npsLrelDlSnNklgdeGaralaealks<-
 ++sL +L+L nN + G + e+L+
 15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGLHN 235

FIG. 11H

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
 ->LtnLeeLdlsqNkI....kkiENLde<-
 Lt L++L L +N+I++ +++++E+L++
 15088 209 LTSLVVLHLHNNRIqhlgtHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
 ->PpsLkeLnvsnNrLteLPeL<-
 ++L++L+ ++N+L e+P
 15088 233 LHNLETLDLNYNKLQEFPPVA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L+nL++LdL++N+L++ P + +
 15088 233 LHNLETLDLNYNKLQEFPPVAI-RT 255

LRR_ps_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L++L++LdL++N+L e+P +
 15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 +L+eL+ nN+++ Pe
 15088 256 LGRLQELGFHNNNIKAIEK 275

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
 -->LtsLqvldLsnNnLsGeIPsslgn<-
 L +Lq+L ++nNn+ IP+ +
 15088 256 LGRlQELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
 -->LpnLrelldLsnNqLtsLPpgaFgg<-
 L+ L+eL +nN++++P+ aF g
 15088 256 LGRlQELGFHNNNIKAIPEKAFMG 279

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
 -->LpnLrelldLsnNqLtsLPpgaFgg<-
 ++L+ L L + ++ LP+g++q
 15088 327 TTSLEIILTlTRAGIRLLPSGMCQQ 350

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
 -->PpsLkelnvsnNrLtelPeL<-
 p+L+ L s+N+++eLP L
 15088 351 LPRLRVLELSHNQIEELPSL 370

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
 -->LtsLqvldLsnNnLsGeIPsslgn<-
 L++L+vL+Ls+N++ e+Ps l +
 15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372

FIG. 11J

LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
 ->LtnLeeLdLsqNkIkkiENLde<-
 L +L++L+Ls+N+I+ + L+
 15088 351 LPRLRVLELSHNQIEELPSLHR 372

LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 Lp Lr+L Ls+Nq+++LP + ++
 15088 351 LPRLRVLELSHNQIEELP-SLHRC 373

LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
 ->npsLreLdLsnNklgdeGaraLaealks<-
 +p+Lr+L Ls+N + + + ++ L++
 15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378

LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 +++L+++ L++N++ ++++
 15088 373 CQKLEEIGLQHNRIWEIGADTFSQ 396

LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 +L+e L++N++ ++ +++F+
 15088 374 -QKLEEIGLQHNRIWEIGADTFSQ 396

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdLs+N I++i
 15088 397 LSSLQALDLSWNAIRSIHPEAF 418

LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq LdLs+N + +I ++ ++
 15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L+ LdLs+N+++s++p+aF+
 15088 397 LSSLQALDLSWNAIRSIHPEAFST 420

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
 ->PpsLkeLnvsnNrLtelPeL<-
 +sL +L+ +N+Lt+LP
 15088 421 LHSLVKLDLTDNQLTLPLA 440

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdL +N+++ + L +
 15088 421 LHSLVKLDLTDNQLTLTTL-FLAG 441

FIG. 11L

```

LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
      *->LtsLqvLdLsnNnLsGeIPsslgn<-*
            L+S L+ LdL +N+L+ ++P   g
15088      421      LHSVVKLDLTDNQLT-TLPL-AGL      442

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
      *->LpnLrelLsnNqLtsLPpgaFgg<-*
            L++L +LdL +NqLt+LP   ++g
15088      421      LHSVVKLDLTDNQLTTLPLAGLGG      444

//

```


FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLso_

```

. . . . .
. . . . .
. . . . .

901 CCCACAGCTTCGAGGGGCTGCACAAATCTGGAGACACTAGACCTGAACATAT 950
    |||||
1  .....GGGCTGCACAAATCTGGAGACACTAGACCTGAATTAT 36

. . . . .
. . . . .
. . . . .

951 AATGAGCTGCAGGAGTTCCTTGGCTATCCGGACCCCTGGGCAGACTGCA 1000
    || |||||
37 AACAAAGCTGCAGGAGTTCCTGTGGCCATCCGGACCCCTGGGCAGACTGCA 86

. . . . .
. . . . .
. . . . .

1001 AGAATTGGGTTTCCATAAACAAACATCAAGGCTATCCAGAGAAAGCCT 1050
    ||| |||| |
87 GGAACCTGGGGTTCATAAACAAACATCAAGGCCATCCAGAAAAGGCCT 136

. . . . .
. . . . .
. . . . .

1051 TCATGGGCAACCCCTCTCTGCAGACAATACATTTTATGACAACCCAATC 1100
    ||||| ||||| || ||||| ||||| ||||| |||||
137 TCATGGGGAACCCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186

. . . . .
. . . . .
. . . . .

1101 CAGTTGTGGGAAGGTCAGCATTCAGTACCTGTCTAAACTGCATACGCT 1150
    ||||| ||||| || ||||| ||||| ||||| || ||
187 CAGTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236

```

FIG. 12C

1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCAGACCTCAAAGGCA 1200
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286
 .
 1201 CCACTAGCCTGGAGATCCTGACCCCTGACCCGTGCGGGCATCAGACTGCTC 1250
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 287 CCACCAGCCTGGAGATCCTGACCCCTGACCCCGCAGGCATCCGGCTGCTC 336
 .
 1251 CCACCGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
 ||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 337 CCATCGGGGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGGAACTGTC 386
 .
 1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAAGAGCTGG 1350
 ||| |||| || |||| || |||| |||| |||| |||| |||| ||||
 387 TCACAAATCAAAATTGAGGAGCTGCCAGCCTGCACAGGTGTCAGAAATTGG 436
 .
 1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAATTGGAGCTGACACC 486
 .
 1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536
 .
 1451 CCGTGCCATCCACCCCTGAGGCTTTCTCAACCCCTTCGATCCTTGGTTAAGC 1500
 ||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 537 CCGGTCCATCCACCCCTGAGGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGC 586

1501 TGGACCTGACTGACAAACCAGCTGACCACACTGCCCTGGCTGGCTGGGA 1550
||||| ||||||| ||||||| ||||||| ||||||| |||

587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCTGGCTGGACTTGGG 636

1551 GGCCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGCCCTT 1600
||| ||||||| ||||||| ||||||| ||||||| ||| ||| |||||||

637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTT 686

1601 CTCCAAGGACAGTTTCCAAAACCTGAGGATCCTGGAGGTGCCCTACGCCT 1650
||||| ||||||| ||||||| ||||||| ||||||| ||| |||

687 CTCCAAGGACAGTTTCCAAAACCTGAGGATCCTGGAGGTGCCCTATGCCT 736

1651 ACCAGTGTGTGCCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
||||| ||||||| |||| || ||||||| ||||||| |||||||

737 ACCAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGG 786

1701 CAGTGGCAGGCCGAGGACTTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
||||| |||| || ||| ||||| || ||| ||||||| ||| |||

787 CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG 836

1751 GCCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC 1800
||||| ||||||| ||||||| ||||||| ||||||| ||||| |||||

837 GCCCCCTGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC 886

1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTGTC 1850
||||| ||||||| |||| || ||||||| ||||||| |||||||

887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAAGTGTC 936

1851 CAGTGCAGCCCTGTTCAGGCCCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
937 CAGTGTAGCCCTACTCCAGGCCCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986

1901 GAGCTGGGCATCCGCCCTTGCTGTGTGGCCAATCGTGCTGCTCCTCCGTAC 1950
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
987 AAGCTGGGCATCCGCCCTGGCCGTGTGGGCCCATCGTGTGCTCCTCCGTGC 1036

1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCAGCCCCG 2000
|||| | || ||||| ||||| || || || ||||| || ||||| |||||
1037 TCTGCAATGGACTGGTGCTGCTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCC 1086

2001 CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAAACGCCCT 2050
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1087 CTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTT 1136

2051 GACGGGCATTTCCCTGTGGTCTCCTGGCCTCTGTGGACGCCCTTGACCTATG 2100
||| ||||| ||||| || || ||||| || || ||||| || ||||| |||||
1137 GACTGGCATTTCCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG 1186

2101 GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAG 2150
||||| ||||| ||||| ||||| ||||| ||||| || || ||||| || ||||| |||||
1187 GTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGG 1236

2151 GCTACGGGCTTCCCTGGCTGTCTGGGTTTCAGAGGCCGTGGTGTGCTGCT 2200
|| || ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
1237 GCCACTGGCTTCCCTGGCAGTACTTGGTGGGATCGGAGGCATCGGTGCTGCT 1286

FIG. 12F

2201 CACACTGGCGGCCGTGCAGTGCAGCATCTCTGTGACCCTGCGTCCGAGCCT 2250
||| |||| | ||||||||| ||| || |||| ||||| ||||
1287 CACTCTGGCCGCAGTGCA GTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT 1336

2251 ACGGGAAGCGCGCTGCCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC 2300
| ||||| | || | ||||||| || ||||| | || | ||||
1337 ATGGGAAGTCCCCCTCCCCTGGGCAGCGTTCCAGCAGGGGTCTTAGGCTGC 1386

2301 CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCCGCTGGCCTCGGTGGGAGA 2350
||||| ||||| ||||||||| ||||||| ||||||| |||||||
1387 CTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCTCCCCACTCTGCCCTGCCCTACGCCCCACCCAGGGCCGGC 2400
|| || ||||||||| ||||||||| ||||||||| ||||| ||||| ||||
1437 ATACGGGGCCTCCCCACTCTGCCCTGCCCTACGCCCCACCTGAGGGTCAGC 1486

2401 CGGCCGCCCTGGCCTCGCTGTAGCCCTGGTGATGATGAAC TCGCTCTGC 2450
| || ||||||||| | || ||||||||| ||||||||| |||||
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAAC TCCCTCTGT 1536

2451 TTCCCTGGTGGTGGCCGGCCCTACATCAAGCTCTACTGTGACCTGCCACG 2500
||||||| ||||||| ||||||||| || ||||||||| ||||| |||||
1537 TTCCCTGGTGGTGGCCGGTGCCTACATCAAAC TGTA CTGTGACCTGCCGCG 1586

2501 GGGTGACTTTAGGCCGTGTGGGACTGCGCCA TGGTGC GCCACGTGGCCT 2550
||| ||||||||| ||||||||| ||||||||| ||||| | |||||||||
1587 GGGCGACTTTAGGCCGTGTGGGACTGCGCCA TGGT GAGGCACGTGGCCT 1636

FIG. 12G

2551 GGCTCATCTTTGCAGATGGCCTCCTACTGCCCCGTGGCCTTCTCAGC 2600
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 1637 GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGC 1686
 2601 TTTGCCCTCCATGCTGGGCTTCTTCCCTGTACCCCCGAGGCTGTCAAGTC 2650
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1687 TTCGCCCTCCATGCTGGGCTTCTTCCCTGTACGCCCGAGGCCGTCAAGTC 1736
 2651 AGTCCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTCAACCCACTGCTCT 2700
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1737 TGTCCCTGCTGGTGTGCTGCTGCTGCTGCTGCTCAACCCACTGCTGT 1786
 2701 ACCTGCTCTTCAACCCCTCACTTCCGGGATGACCTCGGGGCTCTGGCCA 2750
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1787 ACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGGGCTTCGGCCC 1836
 2751 AGCCCTCGGTCCCAGGGCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA 2800
 || | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1837 CGCGCAGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGAGCTGGA 1886
 2801 GAAGAGCTCCTGCGACTCCACCCAGCGCTGGTGGCTTCTCAGATGTGG 2850
 ||||| ||||| || || ||||| || ||||| || ||||| || ||||| |||||
 1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936
 2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCCTCTGGGCTAGAGACC 2900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1937 ATCTCATCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACC 1986

3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCCTAACCAATGAGTG 3259
| | | | | | | | | | | | | | | | | | | | |
2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385

3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTCACCCCTG 3306
| | | | | | | | | | | | | | | | | | | | |
2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGCTTCACTTGTGATACTG 2435

3307 GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCCTGGGAAATT 3353
| | | | | | | | | | | | | | | | | | | | |
2436 GGCCCTCTTCCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485

3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAGACAGTGAAGTTATTGGGC 3400
| | | | | | | | | | | | | | | | | | | | |
2486 GTCTGCTTAAGGGAATGAGGGAAG.TAAAGACAGTGAAG.....GGG. 2527

3401 CCTGACAGAGCCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
| | | | | | | | | | | | | | | | | | | | |
2528 ..TG...GAGGGTTGATC...AGGGCACAGTGGACAGGGAGACCTCACA 2568

3450 GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCCTG 3499
| | | | | | | | | | | | | | | | | | | | |
2569 GAGAAAGGC.CTGGAAGGTGATTTC.....CGTGTGACTC..... 2603

3500 TGACATATAGAATATAAAATGTGTTCTGCGTTCCATTAACTTTGACCTAT 3549
| | | | | | | | | | | | | | | | | | | | |
2604 ..ATGGATAGGATACAAAAATGTGTTCCATGTACCATTAACTTTGACATAT 2651

FIG. 12J

3550 GCTGNGCCAAAGTGCTTCCCTGTTAAATAACACTTTTGGAAGACATTGAAAA 3599
|| :|| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
2652 GCCATGCATAAAGACTTCCCTATTAAATAAAGCTTTTGGAAGAGATTAAAAA 2701
3600 AAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGCCGC 3637
|||||
2702 AAAAAAAAAA..... 2711

FIG. 13A

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nC1_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seganal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248
Quality:	3424	Length:	968
Ratio:	4.646	Gaps:	0
Percent Similarity:	90.773	Percent Identity:	89.281

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_May 5, 19100 15:04

..

```

.
.
.

201 IPDYAFQNLTSVLVHLHNNRIQHVGTSHFEGLHNLETLDLNYNELQEFF 250
    |||||
1 .....GLHNLETLDLNYNKLQEFF 19

251 LAIRTLGRLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
    .|||||
20 VAIRTLGRIQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69

301 FQYLSKLHTLSINGATDIQEFFDLKGTTSLEILTLTRAGIRLLPPGVCQ 350
    |||||
70 FQYLPKLHTLSINGAMDIQEFFDLKGTTSLEILTLTRAGIRLLPSGMCQ 119

351 LPRLRIELSHNQIEELPSLHRCQKLEEEIGLRHNRIKEIGADTFSQLGSL 400
    |||||:|||||
120 LPRLRVLELSHNQIEELPSLHRCQKLEEEIGLQHNRIWEIGADTFSQLSSL 169

401 QALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTLPLAGLGGLMHLKL 450
    |||||
170 QALDLSWNAIRSIHPEAFSTLHSLVKDLTDNQLTTLPLAGLGGLMHLKL 219

```



```

801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLWPSPRSPGP 850
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
570 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLPRAGDSGP 619
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 900
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
620 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 669
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

901 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLKAEGATLAGCGS 950
      | | | | | | | | | | : | : | | | | | | | | | | | | | | |
670 LISCQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGL 719
      | | | | | | | | | | : | : | | | | | | | | | | | | | | |

951 SVGGALWPSGSLFASHL* 968
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
720 SGGGGFQPSGLAFASHV* 737
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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FIG. 14A

```
>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCCGGACCGGGAGCGGCAGCTGCGGCCACCGCGCCGTGCG
TCCGCGCCGGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCAGCCGCGGG
GCTCCGGCGCTATGGCTTTTGCGCGCGCTGTGCGTTCGCGAGGCGCGCGGCCCC
CCAGCCCGCCGGGCCACCGCTGCCCGGCCCTGCCACTGCCAGGAGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGCTGTCCGCCGTTCCGGGGACCTGGACCC
CCTGACGGCTTACCCTGGACCTCAGCATGAACAACCTCACAGAGTTTCAGCCTGGCCTCTT
CCACCACCTGCCGCTTCTTGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGCTCTCTACAGCCTGAAATCCTGATGCTGCAGAACAAATCAGCT
GGGAGGAATCCCGCAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCCCTAGA
TGCCAAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCTCCCTCCGCCA
CCTCTGGCTGGACGACAAATGCACTCACGGAGATCCCTGTTCAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCCTGGCCCTCAACCGCATCAGCCACATCCCGACTACGCGTT
CCAGAAATCTCACAGCCTTGTTGGTGTGCTGCAATTGCAATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCCCTGGCAGACTGCAGGAACCTGGGTTCCATAA
CAACAACATCAAGGCCATCCAGAAAAGGCCCTTCATGGGGAACCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAAATCCAGTTTGTGGGAAGATCGGCATTCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACAGCCTGGAGATCCTGACCCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCCAAGCTCCGAGTCCCTGGAACTGTCTCACAAATCAAATTGAGGA
GCTGCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAATCGGCCCTCCAACAACCCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCCTTCTCCACCCTGCACCTCCCTGGTCAA
GCTGGACCTGACAGACAACAGCTGACCACACTGCCCTTGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCC
```


FIG. 14C

AGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
 GCGTCTTGGCCCTGGCTTTCCCTTGGCCCTTCCCTCAGCTTCACTTGATCTGGGCTCTTC
 CTTGTCACTGCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGAAATGA
 GGGAGTAAAGACAGTGAAGGGGTGGAGGTTGATCAGGGCACAGTGGACAGGGAGACCT
 CACARAAAAGGCCCTGGAAGGKGAATTCCTGTGACTCATGGRTAGGAWACAAAATGTG
 TTCCATGTACCATTAATCTTGACATATGCCCATGCATAAARACTTCCCTATTAAAAATAAGCT
 TTGGRAGAGATT

FIG. 15

>15088
 MPSPGLRALWLCASRRAGAPQPGPGTACAPACHCQEDGIMLSADCSEIGLSAVPGDLPLTAYLDLSMNNLT
 ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLQSLRLDANLI SILVPERSE
 EGLSSLRHLWDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVHLHNNRIQHLGTHSFEGLHNLE
 TLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAPEKAFMGNPILQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAM
 DIQEFFDLKGTTSLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFS
 QLSSLQALDLWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGIMHLKIKGNLALSQAFSKDSFPKLRILEVP
 YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPIGLLARQAEENHYDQDLDELQLEMEDSKPHPSVQCSTPGPFK
 PCEYLFESWGIRLAVWAI VLLSVLCNGLVLLTVFAGGPAPLPVPKFFVGAIAAGANTLTGISCGLLASVDALTFGQFSEY
 GARWETGLGCRTGFLAVLGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEY
 GASPLCLPYAPPEGQPAALGFTVALVMNNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVWLI FADGLLYCPVA
 FLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLENPHFRDDLRLRPRAGDSGPLAYAAAAGELEKSSCDSTQA
 LVAFSDVDLILEASEAGRPPGLETYGFPSVTLISCCQPGAPRLEGSHCPEPEGNHFGNPQPSMDGELLILRAEGSTPAGG
 GLSGGGGFQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248

Quality:	4495	Length:	968
Ratio:	4.653	Gaps:	2
Percent Similarity:	91.097	Percent Identity:	89.855

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

FrGcgManager_9_PBA0KqkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

FIG. 16B

1	MHSPPGLLAIWLCAVL	CASARGGSDPPQPG	GRPAC	PAPCHCQEDGIMLSA	50	Mouse
1	MPSPPGILRAIWLCAAL	CASRRAGGAPQPG	PGTAC	PAPCHCQEDGIMLSA	50	Human
51	DCSELGLSVVPADLDPL	TAYLDLSMNLT	ELQPGLFHHLRFL	EELRLSGN	100	
51	DCSELGLSAVPGDLDPL	TAYLDLSMNLT	ELQPGLFHHLRFL	EELRLSGN	100	
101	HLSHIPGQAFSGLSL	KILMLQSNQ	LRGIPAEALWELPS	LSLRILDANLI	150	
101	HLSHIPGQAFSGLSL	KILMLQNNQ	LRGIPAEALWELPS	LSLRILDANLI	150	
151	SLVPERSEGLSSLRH	LWLDNALTEIP	VRALNNLPALQAMT	LALNHIRH	200	
151	SLVPERSEGLSSLRH	LWLDNALTEIP	VRALNNLPALQAMT	LALNRIH	200	
201	IPDYAFQNLTSLV	VLHLHNNRIQ	HVGTHSFEGLHNLE	TLDLNYNELQEFF	250	
201	IPDYAFQNLTSLV	VLHLHNNRIQ	HVGTHSFEGLHNLE	PLDLNYNKLQEFF	250	
251	LAIRTLGRIQELGF	HNNNIKA	PEKAFMGNPLLQ	TIHFYDNPIQFVGRSA	300	
251	VAIRTLGRIQELGF	HNNNIKA	PEKAFMGNPLLQ	TIHFYDNPIQFVGRSA	300	
301	FQYLSKLHTLSIN	GATDIEFF	DLKGTTSLEILT	LRAGIRLLPPGVCQ	350	
301	FQYLPKLHTLSIN	GAMDIEFF	DLKGTTSLEILT	LRAGIRLLPSGMCQ	350	

FIG. 16C

351 LPRLRILELSHNQIEELPSLHRCQKLEEEIGLRHNRIKEIGADTFSQLGSL 400
 ||||:|||||
 351 LPRLRILELSHNQIEELPSLHRCQKLEEEIGLRHNRIWEIGADTFSQLSSL 400
 401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
 |||||
 401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
 451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFCKTSQWQAEDE 500
 |||||
 451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFCKASQWQAEDEL 500
 501 HPSEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDESKPNPSVQCSPPVG 550
 |::|||
 501 HLDDESSKRPLGLLAGQAENHYDQDLDELQLEMEDESKPHPSVQCSPTPG 550
 551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLIV 598
 |||||
 551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 600
 599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
 |||.|||
 601 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRAATGFLAV 650
 649 LGSEASVLLLTAAVQCSISVTCVRAYGKAPSGSVRAGALGCLALAGLA 698
 |||||
 651 LGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSRAGVLGCLALAGLA 700

FIG. 16D

```

699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMNNSLCFLVVAGA 748
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNNSFCFLVVAGA 750
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

749 YIKLYCDLPRGDFEAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGL 798
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
751 YIKLYCDLPRGDFEAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGL 800
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

799 FPVTPEAVKSVLLVVLPLPACLNPLLYLLENPHFRDDLRLRLWPSRSPGP 848
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLENPHFRDDLRLRLPRAGDSGP 850
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

899 LISRHQPGATRLEGNHFIESDGTKFCGNPQPPMKGELLKAEGATLAGCGS 948
    | | | | | | | | | | : | | | | | | | | | | : | | | | | |
901 LISCCQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGL 950
    | | | | | | | | | | : | | | | | | | | | | : | | | | | |

949 SVGGALWPSGSLFASHL* 966
    | | | | | | | | | |
951 SGGGFGQPSGLAFASHV* 968
    | | | | | | | | | |

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